RAW SEQUENCE LISTING   DATE: 02/06/2002
PATENT APPLICATION: US/09/654,281B   TIME: 08:50:53

Input Set : A:\ES.txt
Output Set: N:\CRF3\02062002\I654281B.raw

ENTERED

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 3 <110> APPLICANT: Sedivy, John
 4         Kolch, Walter
 5         Yeung, Kam Chi
 7 <120> TITLE OF INVENTION: Kinase Inhibitors and Methods of Use in Screening Assays and
Modulation
 8         of Cell Proliferation and Growth
10 <130> FILE REFERENCE: 3564/1010
12 <140> CURRENT APPLICATION NUMBER: 09/654,281B
13 <141> CURRENT FILING DATE: 2000-09-01
15 <150> PRIOR APPLICATION NUMBER: 60/151,992
16 <151> PRIOR FILING DATE: 1999-09-01
18 <160> NUMBER OF SEQ ID NOS: 11
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 94
24 <212> TYPE: PRT
25 <213> ORGANISM: Artificial Sequence
27 <220> FEATURE:
28 <223> OTHER INFORMATION: consensus sequence
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32 <222> LOCATION: (3)..(5)
33 <223> OTHER INFORMATION: Xaa = any amino acid
36 <220> FEATURE:
37 <221> NAME/KEY: MISC_FEATURE
38 <222> LOCATION: (9)..(9)
39 <223> OTHER INFORMATION: a hydrophobic amino acid residue
42 <220> FEATURE:
43 <221> NAME/KEY: MISC_FEATURE
44 <222> LOCATION: (11)..(13)
45 <223> OTHER INFORMATION: Xaa = any amino acid
48 <220> FEATURE:
49 <221> NAME/KEY: MISC_FEATURE
50 <222> LOCATION: (14)..(14)
51 <223> OTHER INFORMATION: a negatively charged amino acid residue
54 <220> FEATURE:
55 <221> NAME/KEY: MISC_FEATURE
56 <222> LOCATION: (15)..(18)
57 <223> OTHER INFORMATION: Xaa = any amino acid residue
60 <220> FEATURE:
61 <221> NAME/KEY: MISC_FEATURE
62 <222> LOCATION: (20)..(21)
63 <223> OTHER INFORMATION: Xaa = any amino acid residue
66 <220> FEATURE:
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Input Set : A:\ES.txt
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 68 <222> LOCATION: (23)..(72)
 69 <223> OTHER INFORMATION: Xaa = any amino acid residue, 0 to 40 residues may be missing
 72 <220> FEATURE:
 73 <221> NAME/KEY: MISC_FEATURE
 74 <222> LOCATION: (74)..(77)
 75 <223> OTHER INFORMATION: Xaa = any amino acid residue
 78 <220> FEATURE:
 79 <221> NAME/KEY: MISC_FEATURE
 80 <222> LOCATION: (79)..(82)
 81 <223> OTHER INFORMATION: Xaa = any amino acid residue, 0 to 2 residues may be missing
 84 <220> FEATURE:
 85 <221> NAME/KEY: MISC_FEATURE
 86 <222> LOCATION: (84)..(84)
 87 <223> OTHER INFORMATION: Xaa = any amino acid residue
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 91 <221> NAME/KEY: MISC_FEATURE
 92 <222> LOCATION: (87)..(87)
 93 <223> OTHER INFORMATION: Xaa = an aromatic amino acid residue
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 97 <221> NAME/KEY: MISC_FEATURE
 98 <222> LOCATION: (89)..(89)
 99 <223> OTHER INFORMATION: Xaa = any amino acid residue
102 <220> FEATURE:
103 <221> NAME/KEY: MISC_FEATURE
104 <222> LOCATION: (90)..(90)
105 <223> OTHER INFORMATION: a hydrophobic amino acid residue
108 <220> FEATURE:
109 <221> NAME/KEY: MISC_FEATURE
110 <222> LOCATION: (91)..(93)
111 <223> OTHER INFORMATION: Xaa = any amino acid residue
114 <400> SEQUENCE: 1
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W--> 116 Thr Leu Xaa Xaa Xaa Asp Pro Asp Glx Pro Xaa Xaa Xaa Asx Xaa Xaa
     117 1               5                   10                  15
W--> 120 Xaa Xaa Glu Xaa Xaa His Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     121             20                  25                  30
W--> 124 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     125         35                  40                  45
W--> 128 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
     129     50                  55              60
W--> 132 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Xaa Xaa Pro Xaa Xaa
     133 65                  70              75                  80
W--> 136 Xaa Xaa Gly Xaa His Arg Xaa Val Xaa Glx Xaa Xaa Xaa Gln
     137             85                  90
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141 <211> LENGTH: 187
142 <212> TYPE: PRT
143 <213> ORGANISM: Homo sapiens
145 <400> SEQUENCE: 2
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Input Set : A:\ES.txt
Output Set: N:\CRF3\02062002\I654281B.raw

```
147 Met Pro Val Asp Leu Ser Lys Trp Ser Gly Pro Leu Ser Leu Gln Glu
148 1               5                   10              15
151 Val Asp Glu Gln Pro Gln His Pro Leu His Val Thr Tyr Ala Gly Ala
152             20              25              30
155 Ala Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Lys Asn
156         35              40              45
159 Arg Pro Thr Ser Ile Ser Trp Asp Gly Leu Asp Ser Gly Lys Leu Tyr
160     50              55              60
163 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
164 65              70              75              80
167 Tyr Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
168             85              90              95
171 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
172             100             105             110
175 Lys Gly Thr Gly Leu His Arg Tyr Val Trp Leu Val Tyr Glu Gln Asp
176         115             120             125
179 Arg Pro Leu Lys Cys Asp Glu Pro Ile Leu Ser Asn Arg Ser Gly Lys
180     130             135             140
183 His Arg Gly Lys Phe Lys Val Ala Ser Phe Arg Lys Lys Tyr Glu Leu
184 145             150             155             160
187 Arg Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Lys Lys Tyr
188             165             170             175
191 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
192             180             185
195 <210> SEQ ID NO: 3
196 <211> LENGTH: 187
197 <212> TYPE: PRT
198 <213> ORGANISM: Mus musculus
200 <220> FEATURE:
201 <221> NAME/KEY: MISC_FEATURE
202 <222> LOCATION: (150)..(150)
203 <223> OTHER INFORMATION: Xaa = any amino acid residue
206 <400> SEQUENCE: 3
208 Met Ala Ala Asp Ile Ser Gln Trp Ala Gly Pro Leu Cys Leu Gln Glu
209 1               5                   10              15
212 Val Asp Glu Pro Pro Gln His Ala Leu Arg Val Asp Tyr Ala Gly Val
213             20              25              30
216 Thr Val Asp Glu Leu Gly Lys Val Leu Thr Pro Thr Gln Val Met Asn
217         35              40              45
220 Arg Pro Ser Ser Ile Ser Trp Asp Gly Leu Asp Pro Gly Lys Leu Tyr
221     50              55              60
224 Thr Leu Val Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Asp Pro Lys
225 65              70              75              80
228 Phe Arg Glu Trp His His Phe Leu Val Val Asn Met Lys Gly Asn Asp
229             85              90              95
232 Ile Ser Ser Gly Thr Val Leu Ser Asp Tyr Val Gly Ser Gly Pro Pro
233             100             105             110
236 Ser Gly Thr Ser Ile His Arg Tyr Val Trp Leu Val Tyr Glu Gln Glu
237         115             120             125
```

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Input Set : A:\ES.txt
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```
240 Gln Pro Leu Ser Cys Asp Glu Pro Ile Leu Ser Asn Lys Ser Gly Asp
241      130              135·             140
244 Asn Arg Gly Lys Phe Xaa Val Glu Thr Phe Arg Lys Lys Tyr Asn Leu
245 145             150              155             160
248 Gly Ala Pro Val Ala Gly Thr Cys Tyr Gln Ala Glu Trp Asp Asp Tyr
249             165              170             175   .
252 Val Pro Lys Leu Tyr Glu Gln Leu Ser Gly Lys
253             180              185
256 <210> SEQ ID NO: 4
257 <211> LENGTH: 187     .
258 <212> TYPE: PRT
259 <213> ORGANISM: Drosophila
261 <400> SEQUENCE: 4.
263 Met Ser Asp Ser Thr Val Cys Phe Ser Lys His Lys Ile Val Pro Asp
264 1             5              10             15
267 Ile Leu Lys Thr Cys Pro Ala Thr Leu Leu Thr Val Thr Tyr Gly Gly
268   .           20              25             ·30
271 Gly Gln Val Val Asp Val Gly Gly Glu Leu Thr Pro Thr Gln Val Gln
272         35              40              45
275 Ser Gln Pro Lys Val Lys Trp Asp Ala Asp Pro Asn Ala Phe Tyr Thr
276      50              55              60
279 Leu Leu Leu Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu Pro Lys Phe
280 65              70              75              80
283 Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly Asn Gln Val
284             85              90              95
287 Glu Asn Gly Val Val Leu Thr Glu Tyr Val Gly Ala Gly Pro Pro Gln
288             100             105             110
291 Gly Thr Gly Leu His Arg Tyr Val Phe Ile Val Phe Lys Gln Pro Gln
292         115             120             125
295 Lys Leu Thr Cys Asn Glu Pro Lys Ile Pro Lys Thr Ser Gly Asp Lys
296      130             135             140 ·
299 Arg Ala Asn Phe Ser Thr Ser Lys Phe Met Ser Lys Tyr Lys Leu Gly
300 145             150             155             160
303 Asp Pro Ile Ala Gly Asn Phe Phe Gln Ala Gln Trp Asp Asp Tyr Val
304             165             170             175
307 Pro Lys Leu Tyr Lys Gln Leu Ser Gly Lys Lys
308             180             185
311 <210> SEQ ID NO: 5
312 <211> LENGTH: 220
313 <212> TYPE: PRT
314 <213> ORGANISM: C. elegans
316 <400> SEQUENCE: 5
318 Met Val Val Leu Val Thr Arg Ser Leu Leu Pro Ala Leu Phe Phe Ala
319 1             5              10             15.
322 Ser Arg Ala Pro Phe Ala Ala Ala Thr Thr Ser Ala Arg Phe Gln Arg
323             20              25              30
326 Gly Leu Ala Thr Met Ala Ala Glu Ala Phe Thr Lys His Glu Val Ile
327         35              40              45
330 Pro Asp Val Leu Ala Ser Asn Pro Pro Ser Lys Val Val Ser Val Lys
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PATENT APPLICATION: US/09/654,281B   TIME: 08:50:53

Input Set : A:\ES.txt
Output Set: N:\CRF3\02062002\I654281B.raw

```
331     50                  55                  60
334 Phe Asn Ser Gly Val Glu Ala Asn Leu Gly Asn Val Leu Thr Pro Thr
335 65                  70                  75                  80
338 Gln Val Lys Asp Thr Pro Glu Val Lys Trp Asp Ala Glu Pro Gly Ala
339                 85                  90                  95
342 Leu Tyr Thr Leu Thr Lys Thr Asp Pro Asp Ala Pro Ser Arg Lys Glu
343                 100                 105                 110
346 Pro Thr Tyr Arg Glu Trp His His Trp Leu Val Val Asn Ile Pro Gly
347             115                 120                 125
350 Asn Asp Ile Ala Lys Gly Asp Thr Leu Ser Glu Tyr Ile Gly Ala Gly
351     130                 135                 140
354 Pro Pro Lys Thr Gly Leu His Arg Tyr Val Tyr Leu Ile Tyr Lys Gln
355 145                 150                 155.                160
358 Ser Gly Arg Ile Glu Asp Ala Glu His Gly Arg Leu Thr Asn Thr Ser
359                 165                 170                 175
362 Gly Asp Lys Arg Gly Gly Trp Lys Ala Ala Asp Phe Val Ala Lys His
363             180                 185                 190
366 Lys Leu Gly Ala Pro Val Phe Gly Asn Leu Phe Gln Ala Glu Tyr Asp
367             195                 200                 205
370 Asp Tyr Val Pro Ile Leu Asn Lys Gln Leu Gly Ala
371     210                 215                 220
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374 <210> SEQ ID NO: 6
375 <211> LENGTH: 181
376 <212> TYPE: PRT
377 <213> ORGANISM: Antirrhinum-CEN
379 <400> SEQUENCE: 6

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382 1               5                   10                  15
385 Gly Asp Val Val Asp His Phe Thr Ser Thr Val Lys Met Ser Val Ile
386             20                  25                  30
389 Tyr Asn Ser Asn Asn Ser Ile Lys His Val Tyr Asn Gly His Glu Leu
390         35                  40                  45
393 Phe Pro Ser Ala Val Thr Ser Thr Pro Arg Val Glu Val His Gly Gly
394     50                  55                  60
397 Asp Met Arg Ser Phe Phe Thr Leu Ile Met Thr Asp Pro Asp Val Pro
398 65                  70                  75                  80
401 Gly Pro Ser Asp Pro Tyr Leu Arg Glu His Leu His Trp Ile Val Thr
402             85                  90                  95
405 Asp Ile Pro Gly Thr Thr Asp Ser Ser Phe Gly Lys Glu Val Val Ser
406             100                 105                 110
409 Tyr Glu Met Pro Arg Pro Asn Ile Gly Ile His Arg Phe Val Phe Leu
410         115                 120                 125
413 Leu Phe Lys Gln Lys Lys Arg Gly Gln Ala Met Leu Ser Pro Pro Val
414     130                 135                 140
417 Val Cys Arg Asp Gly Phe Asn Thr Arg Lys Phe Thr Gln Glu Asn Glu
418 145                 150                 155                 160
421 Leu Gly Leu Pro Val Ala Ala Val Phe Phe Asn Cys Gln Arg Glu Thr
422             165                 170                 175
425 Ala Ala Arg Arg Arg
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Use of n and/or Xaa has been detected in the Sequence Listing.
Review the Sequence Listing to insure a corresponding
explanation is presented in the <220> to <223> fields of
each sequence using n or Xaa.

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                    VERIFICATION SUMMARY                DATE: 02/06/2002
                    PATENT APPLICATION:  US/09/654,281B    TIME: 08:50:54

                    Input Set : A:\ES.txt
                    Output Set: N:\CRF3\02062002\I654281B.raw

L:116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:128 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:136 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:244 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:561 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:10
L:575 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:581 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:11
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